

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,840  
Source: PCT  
Date Processed by STIC: 06-22-2005

***ENTERED***



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/538,840

DATE: 06/22/2005  
TIME: 10:15:14

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\06222005\J538840.raw

3 <110> APPLICANT: N. V. Nutricia  
 4 Schmitt, Joachim  
 5 Boehm, GOonther  
 6 Stahl, Bernd  
 7 Schauer, Roland  
 8 Tiralongo, Evelin  
 9 Schrader, Silke  
 11 <120> TITLE OF INVENTION: Trans-Sialidases obtained from Trypanosoma congolense  
 13 <130> FILE REFERENCE: NUT-047-WO  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/538,840  
 C--> 15 <141> CURRENT FILING DATE: 2005-06-13  
 15 <150> PRIOR APPLICATION NUMBER: DE 10258400.1  
 16 <151> PRIOR FILING DATE: 2002-12-13  
 18 <160> NUMBER OF SEQ ID NOS: 4  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1491  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Trypanosoma congolense  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(1491)  
 30 <223> OTHER INFORMATION:  
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 34 Thr Asp Thr Val Ala Lys Tyr Ser Thr Asp Gly Gly Arg Thr Trp Lys  
 35 1 5 10 15  
 37 agg gag gtt ata att ccg aat ggt cgt gtg gat gcc cac tac tcc cgc 96  
 38 Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg  
 39 20 25 30  
 41 gtc gtt gat ccc act gtt gcg aag ggt aat aac att tat gtt ctc 144  
 42 Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu  
 43 35 40 45  
 45 gtt ggg cgg tac aat gtc acg cgg ggc tac tgg cac aat agg aac aac 192  
 46 Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn  
 47 50 55 60  
 49 aag gct ggc ata gcc gat tgg gag ccc ttc gtg tac aag ggc acg gtg 240  
 50 Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val  
 51 65 70 75 80  
 53 aac gtg ggc acg aag ggc aat gcc act gat gtg tcg atc acg tgg gag 288  
 54 Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu  
 55 85 90 95  
 57 agg act gca ctg aag tcg ctg tac aac ttc cgg gtt tcg gga acg cct 336

(Pg-6)

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58	Arg	Thr	Ala	Leu	Lys	Ser	Leu	Tyr	Asn	Phe	Pro	Val	Ser	Gly	Ser	Pro	
59			100				105						110				
61	ggc	acg	cag	ttc	ctt	gga	ggg	gct	ggg	ggt	ggt	gtt	gta	aca	tcc	aac	384
62	Gly	Thr	Gln	Phe	Leu	Gly	Gly	Ala	Gly	Gly	Gly	Val	Val	Thr	Ser	Asn	
63			115				120					125					
65	ggg	acg	att	gtg	ctg	cca	gtg	cag	gca	agg	aac	aag	gcc	aac	cgt	gtt	432
66	Gly	Thr	Ile	Val	Leu	Pro	Val	Gln	Ala	Arg	Asn	Lys	Ala	Asn	Arg	Val	
67			130				135				140						
69	gtg	agc	atg	atc	ctg	tac	tcg	gct	gac	gat	gga	aag	tca	tgg	cac	ttt	480
70	Val	Ser	Met	Ile	Leu	Tyr	Ser	Ala	Asp	Asp	Gly	Lys	Ser	Trp	His	Phe	
71	145			150				155			160						
73	ggg	aag	ggt	gag	gcc	ggt	gta	ggc	acg	tcc	gag	gct	gcc	ctc	act	gag	528
74	Gly	Lys	Gly	Glu	Ala	Gly	Val	Gly	Thr	Ser	Glu	Ala	Ala	Leu	Thr	Glu	
75			165				170				175						
77	tgg	gac	ggc	aag	ctg	ctg	att	agt	gca	cga	tcc	gat	ggg	cag	ggc		576
78	Trp	Asp	Gly	Lys	Leu	Leu	Ile	Ser	Ala	Arg	Ser	Asp	Gly	Gly	Gln	Gly	
79			180				185				190						
81	tac	cgc	atg	ata	ttc	gaa	tcg	agt	gac	ctt	ggt	gcg	acg	tgg	aaa	gag	624
82	Tyr	Arg	Met	Ile	Phe	Glu	Ser	Ser	Asp	Leu	Gly	Ala	Thr	Trp	Lys	Glu	
83			195				200				205						
85	atg	ctc	aac	agc	atc	tcc	cgc	gtg	att	ggc	aac	tct	ccg	ggt	cgc	agt	672
86	Met	Leu	Asn	Ser	Ile	Ser	Arg	Val	Ile	Gly	Asn	Ser	Pro	Gly	Arg	Ser	
87			210				215				220						
89	ggt	cct	ggc	agc	tcg	agt	ggc	ttc	atc	acg	gtg	aca	gtg	gag	ggt	gtg	720
90	Gly	Pro	Gly	Ser	Ser	Ser	Gly	Phe	Ile	Thr	Val	Thr	Val	Glu	Gly	Val	
91	225			230				235				240					
93	cct	gtg	atg	ctg	att	acc	cac	ccg	aag	aac	ctt	aag	ggc	tcg	tat	tat	768
94	Pro	Val	Met	Leu	Ile	Thr	His	Pro	Lys	Asn	Leu	Lys	Gly	Ser	Tyr	Tyr	
95			245				250				255						
97	cgg	gac	cgt	ctg	cag	ctg	tgg	atg	acg	gac	ggc	aat	cgt	atg	tgg	cat	816
98	Arg	Asp	Arg	Leu	Gln	Leu	Trp	Met	Thr	Asp	Gly	Asn	Arg	Met	Trp	His	
99			260				265				270						
101	gtc	ggg	cag	gtc	tct	gag	ggc	gac	gat	aac	agc	gct	tac	agc	tcc	ctg	864
102	Val	Gly	Gln	Val	Ser	Glu	Gly	Asp	Asp	Asn	Ser	Ala	Tyr	Ser	Ser	Leu	
103			275				280				285						
105	ctg	tac	act	ccg	gac	ggg	gtc	ctg	tac	tgc	ttg	cat	gag	cag	aac	att	912
106	Leu	Tyr	Thr	Pro	Asp	Gly	Val	Leu	Tyr	Cys	Leu	His	Glu	Gln	Asn	Ile	
107			290				295				300						
109	gat	gag	gtg	tac	agc	ctc	cac	ctt	gtg	cgc	ctt	gtg	gac	gag	ctg	aaa	960
110	Asp	Glu	Val	Tyr	Ser	Leu	His	Leu	Val	Arg	Leu	Val	Asp	Glu	Leu	Lys	
111	305			310				315				320					
113	agc	att	aaa	tca	acg	gct	ctg	gtg	tgg	aag	gca	cag	gac	gag	ctt	ctc	1008
114	Ser	Ile	Lys	Ser	Thr	Ala	Leu	Val	Trp	Lys	Ala	Gln	Asp	Glu	Leu	Leu	
115			325				330				335						
117	ctg	ggc	aac	tgc	ctc	ccg	ggc	gat	aaa	tac	gat	ccc	ggg	tgt	gac	ggc	1056
118	Leu	Gly	Asn	Cys	Leu	Pro	Gly	Asp	Lys	Tyr	Asp	Pro	Gly	Cys	Asp	Gly	
119			340				345				350						
121	atc	ccc	acc	gct	ggg	ctt	gcc	ggg	ctg	ctg	gta	gga	ccc	ctg	acg	gag	1104
122	Ile	Pro	Thr	Ala	Gly	Leu	Ala	Gly	Leu	Leu	Val	Gly	Pro	Leu	Thr	Glu	

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123	355	360	365	
125	aag acg tgg ccc gac gcg tat	cgg tgc gtg aac gct	gca acc agc ggc	1152
126	Lys Thr Trp Pro Asp Ala	Tyr Arg Cys Val Asn Ala	Ala Thr Ser Gly	
127	370	375	380	
129	gct gtg agc act gct gaa	ggc gtg cgg ctg gac	gtg ggt ggc ggt ggc	1200
130	Ala Val Ser Thr Ala	Glu Gly Val Arg Leu Asp	Val Gly Gly Gly	
131	385	390	395	400
133	cat gtt gtg tgg ccc gtg	agt gag cag ggg cag gac	cag cgg tat tac	1248
134	His Val Val Trp Pro Val	Ser Glu Gln Gly Gln Asp	Gln Arg Tyr Tyr	
135	405	410	415	
137	ttt acc aac agc gag ttc	acg ctc gcc gtc acg	gtg cgg ttt gac gag	1296
138	Phe Thr Asn Ser Glu Phe	Thr Leu Ala Val Thr Val	Arg Phe Asp Glu	
139	420	425	430	
141	atg cca cgg ggg gag ctc	ccg ttg ctg ggg ttt	gtg aac cgc aaa ggg	1344
142	Met Pro Arg Gly Glu Leu	Pro Leu Leu Gly Phe Val	Asn Arg Lys Gly	
143	435	440	445	
145	aag gtg aag aag ata ctg	aag gtg tcg ctg agc	ggg gtg gag tgg ctc	1392
146	Lys Val Lys Lys Ile Leu	Lys Val Ser Leu Ser Gly	Val Glu Trp Leu	
147	450	455	460	
149	ctg gca tac ggg aat gag	tac aac agc aca gcc	gct gag ccg ctg gac	1440
150	Leu Ala Tyr Gly Asn Glu	Tyr Asn Ser Thr Ala Ala	Glu Pro Leu Asp	
151	465	470	475	480
153	gtg aac gag agc cac cag	gtg gtg cta gcg ctt	cac gac ggg atc gtc	1488
154	Val Asn Glu Ser His Gln	Val Val Leu Ala Leu His	Asp Gly Ile Val	
155	485	490	495	
157	tcc			1491
158	Ser			
162	<210> SEQ ID NO: 2			
163	<211> LENGTH: 497			
164	<212> TYPE: PRT			
165	<213> ORGANISM: Trypanosoma congolense			
167	<400> SEQUENCE: 2			
169	Thr Asp Thr Val Ala Lys Tyr Ser Thr Asp Gly Gly Arg Thr Trp Lys			
170	1	5	10	15
173	Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg			
174	20	25	30	
177	Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu			
178	35	40	45	
181	Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn			
182	50	55	60	
185	Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val			
186	65	70	75	80
189	Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu			
190	85	90	95	
193	Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro			
194	100	105	110	
197	Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn			
198	115	120	125	
201	Gly Thr Ile Val Leu Pro Val Gln Ala Arg Asn Lys Ala Asn Arg Val			

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202	130	135	140
205	Val Ser Met Ile Leu Tyr Ser Ala Asp Asp Gly Lys Ser Trp His Phe		
206	145	150	155
209	Gly Lys Gly Glu Ala Gly Val Gly Thr Ser Glu Ala Ala Leu Thr Glu		160
210	165	170	175
213	Trp Asp Gly Lys Leu Leu Ile Ser Ala Arg Ser Asp Gly Gly Gln Gly		
214	180	185	190
217	Tyr Arg Met Ile Phe Glu Ser Ser Asp Leu Gly Ala Thr Trp Lys Glu		
218	195	200	205
221	Met Leu Asn Ser Ile Ser Arg Val Ile Gly Asn Ser Pro Gly Arg Ser		
222	210	215	220
225	Gly Pro Gly Ser Ser Gly Phe Ile Thr Val Thr Val Glu Gly Val		
226	225	230	235
229	Pro Val Met Leu Ile Thr His Pro Lys Asn Leu Lys Gly Ser Tyr Tyr		240
230	245	250	255
233	Arg Asp Arg Leu Gln Leu Trp Met Thr Asp Gly Asn Arg Met Trp His		
234	260	265	270
237	Val Gly Gln Val Ser Glu Gly Asp Asp Asn Ser Ala Tyr Ser Ser Leu		
238	275	280	285
241	Leu Tyr Thr Pro Asp Gly Val Leu Tyr Cys Leu His Glu Gln Asn Ile		
242	290	295	300
245	Asp Glu Val Tyr Ser Leu His Leu Val Arg Leu Val Asp Glu Leu Lys		
246	305	310	315
249	Ser Ile Lys Ser Thr Ala Leu Val Trp Lys Ala Gln Asp Glu Leu Leu		320
250	325	330	335
253	Leu Gly Asn Cys Leu Pro Gly Asp Lys Tyr Asp Pro Gly Cys Asp Gly		
254	340	345	350
257	Ile Pro Thr Ala Gly Leu Ala Gly Leu Leu Val Gly Pro Leu Thr Glu		
258	355	360	365
261	Lys Thr Trp Pro Asp Ala Tyr Arg Cys Val Asn Ala Ala Thr Ser Gly		
262	370	375	380
265	Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly		
266	385	390	395
269	His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr		400
270	405	410	415
273	Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu		
274	420	425	430
277	Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly		
278	435	440	445
281	Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu		
282	450	455	460
285	Leu Ala Tyr Gly Asn Glu Tyr Asn Ser Thr Ala Ala Glu Pro Leu Asp		
286	465	470	475
289	Val Asn Glu Ser His Gln Val Val Leu Ala Leu His Asp Gly Ile Val		480
290	485	490	495
293	Ser		
297	<210> SEQ ID NO: 3		
298	<211> LENGTH: 831		
299	<212> TYPE: DNA		

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300 <213> ORGANISM: Trypanosoma congolense  
 302 <220> FEATURE:  
 303 <221> NAME/KEY: CDS  
 304 <222> LOCATION: (1)..(831)  
 305 <223> OTHER INFORMATION:  
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 309 Phe Arg Ile Pro Ser Leu Val Glu Ile Asp Gly Val Leu Ile Ala Thr  
 310 1 5 10 15  
 312 ttc gat aca cgt tat ctt cgc gct tcc gac agc agt ctc ata gac aca 96  
 313 Phe Asp Thr Arg Tyr Leu Arg Ala Ser Asp Ser Ser Leu Ile Asp Thr  
 314 20 25 30  
 316 gct atg aaa tac agt gcc gat cag ggg aag acg tgg aaa act gaa atc 144  
 317 Ala Met Lys Tyr Ser Ala Asp Gln Gly Lys Thr Trp Lys Thr Glu Ile  
 318 35 40 45  
 320 ata ata aaa aat gct aga cta act gat aac ttt tcc cgc gtc gtt gat 192  
 321 Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp  
 322 50 55 60  
 324 cca acg gtt gtt aag ggt gat aac ttg ttt att ttt gtt ggg agg 240  
 325 Pro Thr Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg  
 326 65 70 75 80  
 328 tac aac acc tca tct gcc cca tgg gtc tgg cag gaa aac ggt aaa gac 288  
 329 Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp  
 330 85 90 95  
 332 tgg gat gta ctg ttg tac aag gcc aag gtg agg aag gaa tca gcg ggt 336  
 333 Trp Asp Val Leu Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly  
 334 100 105 110  
 336 ggg gta cca tca gtg agc ttt aca tgg gac gaa ccc cta tac ctg aag 384  
 337 Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys  
 338 115 120 125  
 340 cat ctg ctc acc tct gtc ggt aaa ata gac ggc agg tcc ctc ata caa 432  
 341 His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln  
 342 130 135 140  
 344 tac att ggt ggc gtt gga aat ggt att gta aca ccg aaa ggt act atc 480  
 345 Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile  
 346 145 150 155 160  
 348 gtg ttt cca gtt cag gtt tta aac acc aac aaa tcc gtc atg aac atg 528  
 349 Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met  
 350 165 170 175  
 352 ctt ctg tat tca agt aac gac gga aaa acc tgg gag ttc agc aaa act 576  
 353 Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr  
 354 180 185 190  
 356 tcc aca ccc gcg ggc aca act gag gcc tcc ctt gtt tgg tgg gat gga 624  
 357 Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly  
 358 195 200 205  
 360 caa cta ctt ctc aca agc aga aca act ccg gat gtc ggc agc cgc aaa 672  
 361 Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys  
 362 210 215 220  
 364 gta tat tta aca agc gac ctc gga act tca tgg aat gaa gcg atc gga 720

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30

L:307 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:305